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RESEARCH ARTICLE

Phenotypic Characterization Reveals High Extent of Genetic Variation in Maize (*Zea mays* L.) Landraces of North-Eastern and North-Western Himalayan Regions of India

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Maize (*Zea mays* L.) is an important cereal crop with multiple uses as food, feed, fodder, fuel and biofuel. Phenotypic characterization of newly collected germplasm is essential for selecting genetically diverse lines for maize breeding. We characterized 99 landrace germplasm accessions collected from India's maize diversity hotspots located in North-Eastern Himalayan (NEH) and North-Western Himalayan (NWH) regions using 30 morphological traits. The high extent of phenotypic variation was observed both in plant and ear traits. Landrace accessions displayed desirable traits for earliness and yield contributing traits namely leaf length and width, ear length and width, kernel rows and kernels per row. Very high positive correlations estimated between flowering traits (days to tasseling and silking; r = 0.99) and maturity (0.78), and between plant height and ear height (0.90). However, kernels per row showed significantly negative correlations with flowering traits (-0.42) and maturity (-0.44). Cluster analysis grouped all 99 landrace accessions into eight clusters. Principal component biplot explained 88.24% variation. Boxplot analysis indicated that the maize landrace accessions from NWH region displayed comparatively high phenotypic diversity for plant phenology and architecture traits, while the accessions from NEH region showed the higher variation for tassel branching, ear number, ear width, kernels per row and 100-seed weight. Maize accessions expressed phenotypic variability for all qualitative traits with leaf colour, silk colour and ear shape showing the maximum variation. Shannon-Weaver diversity indices revealed the presence of high phenotypic variation for tassel branching (SDI = 0.99), ear shape, husk cover, ear width, kernel rows (0.95) and kernels per row (0.69). This genepool of landraces offers prospects for pre-breeding by providing new sources of allelic variation to enrich elite maize germplasm.

Key Words: Genetic variation, Himalayan region, India, Maize landraces, Phenotypic characterization

Introduction

Cereals are an important part of food resources for human beings and animals. Maize (*Zea mays* L.) being a main cereal crop has diverse uses as human food, animal feed and fodder, fuel and industrial by-products including biofuel production among all the cereals. It is considered the major staple food in the world and one of the most cultivated among the cereals (Shiferaw *et al*., 2011). It occupies an important position in the world economy and traded as a food, feed and industrial crop. With its higher content of carbohydrates, fats, proteins and some of the important vitamins and minerals, the crop has acquired a well-deserved status as a poor man's 'nutricereal' (Prasanna *et al*., 2001). Recently, global maize production has reached 1147.62 million tonnes (mt) from an area of 193.73 m ha and India produced 27.8 mt from 9.3 m ha (FAO Stat., 2018). This production and productivity needs to improve further to feed the burgeoning global population. Utilization of diverse maize germplasm to enhance the genetic base of donor lines is crucial for the development of new heterotic hybrids and to increase productivity level. Besides the use of new germplasm collections, exploitation of the existing genetic variation of global genebanks is fundamental for the success of crop breeding programmes (Tanksley and McCouch, 1997; McCouch *et al*., 2013).

Landraces constitute an important germplasm, not only well-adapted to the region in which these had

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*Author for Correspondence: Email- mahesh.yadav1@icar.gov.in evolved but also differ in details as to specific adaptation to the particular conditions within the environment (Harlan, 1975a, b). Popularly referred to as 'local varieties' or 'farmer's varieties', the landraces form genetically diverse and heterogeneous populations, which were typically selected by farmers for their adaptation to specific environments, variation in their characteristics like prolificacy, flowering behavior, yield, nutritive value and resistance to biotic and abiotic stresses (Zeven, 1998; Villa *et al*., 2005). They have evolved under subsistence agriculture and are still being cultivated by farmers in regions of crop domestication and diversity (Louette and Smale, 2000; Rojas-Barrera *et al*., 2019). Existence of a vast array of landraces in maize has provided ample opportunities for enriching the allelic diversity and to search for new resources of rare alleles (Prasanna and Sharma, 2005; Warburton *et al*., 2008; Hölker *et al*., 2019). However, genetic resources used in maize breeding programmes around the world represent ~10% of all landraces indicating that much of the genetic diversity remains to be efficiently and effectively explored and exploited. Further, the improved cultivars for higher yield, better quality, disease and pest resistance, and climate-resilience can be developed by using these genetic resources (Dowswell *et al*., 1996; McCouch *et al*., 2020).

The proper knowledge of agro-morphological traits and their genetics will be helpful for better conservation and utilization of such germplasm resources (Nass *et al*., 1993). Extensive variability in plant, ear and tassel characteristics is present in North-Eastern Himalayan (NEH) and North-Western Himalayan (NWH) regions as compared to relatively less varietal diversity existing in the plains of India (Prasanna, 2010). The social and cultural values of the tribes living in the NEH region played an important role in the conservation of maize landraces (Singh, 1977). The NEH region of India comprising states of Arunachal Pradesh, Assam, Nagaland, Manipur, Mizoram, Tripura, Meghalaya, Sikkim and areas in the Northern region of West Bengal possesses huge genetic diversity with respect to plant type, ear traits, quality and resistance to biotic and abiotic stresses (Prasanna and Sharma, 2005; Prasanna, 2012). The racial diversity of maize in India was studied by Grant and Wellhausen (1955) and they observed extensive variability in plant, tassel and ear characteristics in the NEH region and North-Western highlands in India. Extensive studies on the variability of maize in the NEH regions were carried out by Singh (1977). The presence of enormous maize diversity in this region had prompted Stonor and Anderson (1949) to propose an Asiatic origin of maize. For proper utilization of maize genetic resources in breeding programmes, morphological characterization is the first step for the assessment, description and classification of germplasm collections. The importance of phenotyping maize landraces has been highlighted by various studies across the globe (Hartings *et al*., 2008; Salazar *et al*., 2016; Belalia *et al*., 2019; Nelimor *et al*., 2019). Therefore, the aims of present study were i) to characterize maize landrace accessions from NEH and NWH regions of India for their morphological traits and ii) to analyze the extent of phenotypic variation present among the maize accessions for their exploitation in future crop improvement programmes.

Materials and Methods

Germplasm Materials and Field Experimentation

The materials comprising 99 maize landrace accessions and representing 10 different states of NEH and NWH regions of India, were used in the present study (Tables 1, 2). The seeds of maize accessions were obtained from working collection of National Gene Bank at Indian Council of Agricultural Research (ICAR)-National Bureau of Plant Genetic Resources (NBPGR), New Delhi. The geographical coordinates for individual accession were mapped using the information on village, district and state of collection sites through the software 'DIVA-GIS' (Hijmans *et al*. 2001) (Fig. 1). The experiment was laid out in Augmented Block Design (ABD) with four checks namely LM-13 (C-1; Inbred line), LM-14 (C-2; Inbred line), Prabhat (C-3; Composite variety) and PMH-1 (C-4; hybrid cultivar), replicated five times under normal sown irrigated conditions at NBPGR Experimental Farm, New Delhi over two years during *Kharif* seasons of 2017 and 2018. The experimental farm, with sandy loam soil and pH 7.8, is situated at 28°40' N latitude, 77°12' E longitude and 228 m altitude. The mean annual rainfall was 650 mm, of which more than 80% occurred during the south-west monsoon season (July-Sept.) with mean annual evaporation of 850 mm. Each block contained 20 germplasm accessions and four checks, which were randomized. All 99 germplasm accessions were grown in five ABD blocks with individual accession was planted in a two-row plot of 2.5 m length with row to row and plant to plant distances of 60 cm and 20 cm, respectively.

Table 1. Description of germplasm accessions - IC (Indigenous Collection) number, village, district and geographical coordinates of their collection sites located in 10 different states of India

S. No.	Accession Code	IC Number	Village and District of collection site	Geographical Coordinates (Latitude and Longitude)	State Name
1	MA201	IC077261	Sirmour, Sirmaur	30°30' N 77°12' E	Himachal Pradesh
2.	MA202	IC077390	Gool Udhampur, Jammu	32°43' N 74°51' E	Jammu and Kashmir
3.	MA203	IC077463	Jalna, Bageshwar	29°50' N 79°46' E	Uttarakhand
4.	MA204	IC077089	Dilsigiri,West Garo Hills	25°27' N 90°19' E	Meghalaya
5.	MA205	IC077126	Musubai, East Khasi Hills	25°22' N 91°45' E	Meghalaya
6.	MA206	IC077181	Thana, Bilaspur	31°22' N 76°42' E	Himachal Pradesh
7.	MA207	IC083103	Chotolongket, Dima Hasao	25°21' N 91°01' E	Assam
8.	MA208	IC083125	Singrib, West Kameng	27°13' N 92°13' E	Arunachal Pradesh
9.	MA209	IC083146	Chipiketa, Phek	25°41' N 94°27' E	Nagaland
10.	MA210	IC083153	Pikhbasa, Zunheboto	26°03' N 94°34' E	Nagaland
11.	MA211	IC097882	Asgarh, Pauri Garhwal	30°09' N 78°46' E	Uttarakhand
12.	MA212	IC097900	Paunti, Uttarkashi	30°52' N 78°05' E	Uttarakhand
13.	MA213	IC097918	Mashik, Dehradun	30°19' N 78°01' E	Uttarakhand
14.	MA214	IC097936	Barakat, Dehradun	30°19' N 78°01' E	Uttarakhand
15.	MA215	IC097965	Kotala, Hamirpur	31°41' N 76°31' E	Himachal Pradesh
16.	MA216	IC098131	Thambang, North Sikkim	27°31' N 88°30' E	Sikkim
17.	MA217	IC098133	Dhangkey, North Sikkim	27°34' N 88°28' E	Sikkim
18.	MA218	IC098274	Dhoot Patwa, Una	31°38' N 76°59' E	Himachal Pradesh
19.	MA219	IC098165	Moorang, Kinnaur	31°36' N 78°24' E	Himachal Pradesh
20.	MA220	IC109664	Mcleodganj, Kangra	32°13' N 76°19' E	Himachal Pradesh
21.	MA221	IC128762	Amrigok Hills, East Khasi Hills	25°22' N 91°45' E	Meghalaya
22.	MA222	IC128768	South Kolasib, Kolasib	24°13' N 92°40' E	Mizoram
23.	MA223	IC128788	Keithlamtur, Senapati	25°12' N 94°02' E	Manipur
24.	MA224	IC128792	Jaluki, Kohima	25°39' N 94°06' E	Nagaland
25.	MA225	IC128844	Kawnpui, Kolasib	24°03' N 92°39' E	Mizoram
26.	MA226	IC108162	Chamder, Mandi	31°35' N 76°55' E	Himachal Pradesh
27.	MA227	IC108164	Chet, Kullu	31°57' N 77°06' E	Himachal Pradesh
28.	MA228	IC109642	Banthu, Chamba	32°55' N 76°28' E	Himachal Pradesh
29.	MA229	IC130560	Hiralngomun, Aizawl	23°43' N 92°42' E	Mizoram
30.	MA230	IC130596	Sibilon, Tamenglong	24°59' N 93°30' E	Manipur
31.	MA231	IC130605	Bongjong, Chandel	24°18' N 93°35' E	Manipur
32.	MA232	IC130753	Pasighat, East Siang	28°03' N 95°19' E	Arunachal Pradesh
33.	MA233	IC130762	Rengging, East Siang	28°57' N 94°49' E	Arunachal Pradesh
34.	MA234	IC130786	Chododoke, West Siang	28°40' N 94°21' E	Arunachal Pradesh
35.	MA235	IC337348	Khuliya, Champawat	29°20' N 80°05' E	Uttarakhand
36.	MA236	IC278614	Larnoo, Anantnag	33°37' N 75°22' E	Jammu and Kashmir
37.	MA237	IC326557	Budhaal, Rajouri	33°22' N 74°19' E	Jammu and Kashmir
38.	MA238	IC326569	Lassana, Poonch	33°46' N 74°07' E	Jammu and Kashmir
39.	MA239	IC381423	Meleyal, Kupwara	34°07' N 74°10' E	Jammu and Kashmir
40.	MA240	IC393088	Janbila, Bageshwar	29°50' N 79°46' E	Uttarakhand
41.	MA241	IC411752	Tamina Chowkibal, Kupwara	34°10' N 74°03' E	Jammu and Kashmir
42.	MA242	IC411777	Tcharwan Kangan, Srinagar	34°04' N 74°49' E	Jammu and Kashmir
43.	MA243	IC413401	Lazura/Pomepore, Pulwama	33°52' N 74°54' E	Jammu and Kashmir
44.	MA244	IC413449	Zalus/Chadura , Budgam	34°01' N 74°43' E	Jammu and Kashmir
45.	MA245	IC315920	Mudeli, Lower Subansiri	27°49' N 93°31' E	Arunachal Pradesh
46.	MA246	IC281534	Tal, Chamoli	30°30' N 79°09' E	Uttarakhand
47.	MA247	IC281540	Chandhar, Tehri Garhwal	30°24' N 78°28' E	Uttarakhand
48.	MA248	IC338450	Ladflora, Nainital	29°22' N 79°27' E	Uttarakhand
49.	MA249	IC436982	Khaliyan, Rudraprayag	30°28' N 78°55' E	Uttarakhand

S. No.	Accession Code	IC Number	Village and District of collection site	Geographical Coordinates (Latitude and Longitude)	State Name
50.	MA250	IC556406	Bhaderwah, Doda	33°09' N 75°33' E	Jammu and Kashmir
51.	MA251	IC556417	Okuhlu, Ramban	33°25' N 74°28' E	Jammu and Kashmir
52.	MA252	IC556411	Ladder, Kistwar	34°01' N 74°19' E	Jammu and Kashmir
53.	MA253	IC556430	Harsi, Kangra	32°06' N 76°16' E	Himachal Pradesh
54.	MA254	IC556435	Kathla, Hamirpur	31°41' N 76°31' E	Himachal Pradesh
55.	MA255	IC568238	Dadal, Mandi	31°38' N 76°59' E	Himachal Pradesh
56.	MA256	IC568279	Chambi, Kangra	32°06' N 76°16' E	Himachal Pradesh
57.	MA257	IC556413	Ladder, Kistwar	34°12' N 74°21' E	Jammu and Kashmir
58.	MA258	IC556431	Harsi, Kangra	32°06' N 76°16' E	Himachal Pradesh
59.	MA259	IC556434	Kholi, Hamirpur	31°41' N 76°31' E	Himachal Pradesh
60.	MA260	IC550360	Suni, Shimla	31°31' N 77°48' E	Himachal Pradesh
61.	MA261	IC550365	Salooni, Chamba	32°34' N 76°07' E	Himachal Pradesh
62.	MA262	IC526764	Thaltlang, Saiha	22°21' N 93°03' E	Mizoram
63.	MA263	IC526436	Bangtalang, Serchhip	23°20' N 92°51' E	Mizoram
64.	MA264	IC540219	Mongsunyimti, Mokokchung	26°19' N 94°30' E	Nagaland
65.	MA265	IC557452	New Peren, Peren	25°31' N 93°39' E	Nagaland
66.	MA266	IC538895	Mur village, Kurung Kumey	27°34' N 93°12' E	Arunachal Pradesh
67.	MA267	IC526460	Phairuang, Lunglei	22°52' N 92°46' E	Mizoram
68.	MA268	IC524611	Bada Basti, Kohima	25°40' N 94°07' E	Nagaland
69.	MA269	IC524456	Tenyiphe, Dimapur	25°54' N 93°43' E	Nagaland
70.	MA270	IC419530	Pungro, Kiphire	25°49' N 94°51' E	Nagaland
71.	MA271	IC540242	Hakchang, Tuensang	26°18' N 94°51' E	Nagaland
72.	MA272	IC447091	Lower Bomdir, Tawang	27°34' N 91°52' E	Arunachal Pradesh
73.	MA273	IC524478	Sovima, Dimapur	25°54' N 93°43' E	Nagaland
74.	MA274	IC557462	Mokokchung, Mokokchung	26°22' N 94°37' E	Nagaland
75.	MA275	IC540223	Mopungchuket, Mokokchung	26°19' N 94°30' E	Nagaland
76.	MA276	IC527213	Daporijo, Upper Subansiri	27°58' N 94°30' E	Arunachal Pradesh
77.	MA277	IC538976	Pinegrove, Lower Subansiri	27°06' N 93°30' E	Arunachal Pradesh
78.	MA278	IC396886	Tingchim, North Sikkim	27°28' N 88°32' E	Sikkim
79.	MA279	IC412888	Majbat, Darrang	26°27' N 92°01' E	Assam
80.	MA280	IC447153	Kala Pahar, West Kameng	27°17' N 92°24' E	Arunachal Pradesh
81.	MA281	IC540252	Thronger, Tuensang	26°15' N 94°37' E	Nagaland
82.	MA282	IC526679	Sihtlangpui, Lawngtlai	22°18' N 92°42' E	Mizoram
83.	MA283	IC526702	Saiha, Saiha	22°21' N 93°03' E	Mizoram
84.	MA284	IC545332	Kengkhu, Changlang	27°44' N 96°38' E	Arunachal Pradesh
85.	MA285	IC524527	Bade, Dimapur	25°54' N 93°43' E	Nagaland
86.	MA286	IC447215	Merima, Kohima	25°40' N 94°07' E	Nagaland
87.	MA287	IC557454	Old Peren, Peren	25°31' N 93°39' E	Nagaland
88.	MA288	IC538939	Sangram, Kurung Kumey	27°34' N 93°12' E	Arunachal Pradesh
89.	MA289	IC526430	Bangtalang, Serchhip	23°20' N 92°51' E	Mizoram
90.	MA290	IC077124	Musubai, East Khasi Hills	25°22' N 91°45' E	Meghalaya
91.	MA291	IC077192	Daultpur, Una	31°46' N 75°59' E	Himachal Pradesh
92.	MA292	IC077160	Kitpal, Hamirpur	31°41' N 76°31' E	Himachal Pradesh
93.	MA293	IC130593	Sibilon, Tamenglong	24°59' N 93°30' E	Manipur
94.	MA294	IC469859	Sallachigiri, Pithoragarh	29°27' N 80°13' E	Uttarakhand
95.	MA295	IC282853	Bhattagaun, Dehradun	30°25' N 78°04' E	Uttarakhand
96.	MA296	IC469894	Sallalower, Pithoragarh	29°27' N 80°13' E	Uttarakhand
97.	MA297	IC538074	Narsinghdara, Champawat	29°20' N 80°05' E	Uttarakhand
98.	MA298	IC556415	Bankut, Ramban	33°04' N 74°55' E	Jammu and Kashmir
99.	MA299	IC556396	Naltee, Doda	33°09' N 75°55' E	Jammu and Kashmir

Table 2. Name of states, districts, and number of maize landrace germplasm collections characterized morphologically in present study

S. No.	Name of State	Name of District and Number of accessions	Number of Collections
A).	North-Western Himalayan Region (32 Districts)		49
1.	Jammu and Kashmir	Jammu (1), Anantnag (1), Rajouri (1), Poonch (1), Kupwara (2), Srinagar (1), Budgam (1), Pulwama (1), Doda (2), Ramban (2) and Kistwar (2) ; (11 Districts)	15
2.	Himachal Pradesh	Sirmaur (1), Bilaspur (1), Una (2), Kinnaur (1), Kangra (4), Hamirpur (4), Mandi (2), Kullu (1), Chamba (2) and Shimla (1); (10 Districts)	19
3.	Uttarakhand	Pauri Garhwal (1), Uttarkashi (1), Dehradun (3), Champawat (2), Bageshwar (2), Chamoli (1), Tehri Garhwal (1), Nainital (1), Rudraprayag (1) and Pithoragarh (2); (11 Districts)	15
B).	North-Eastern Himalayan Region (30 districts)		50
4.	Sikkim	North Sikkim (3); (1 District)	3
5.	Arunachal Pradesh	West Kameng (2), East Siang (2), West Siang (1), Kurung Kumey (2), Tawang (1), Upper Subansiri (1), Lower Subansiri (2) and Changlang (1); (8 Districts)	12
6.	Nagaland	Phek (1), Zunheboto (1), Kohima (3), Mokokchung (3), Tuensang (2), Dimapur (3), Kiphire (1) and Peren (2); (8 Districts)	16
7.	Manipur	Senapati (1), Tamenglong (2) and Chandel (1); (3 Districts)	4
8.	Mizoram	Kolasib (2), Aizawl (1), Saiha (2), Serchhip (2), Lunglei (1) and Lawngtlai (1); (6 Districts)	9
9.	Meghalaya	West Garo Hills (1), East Khasi Hills (3); (2 Districts)	4
10.	Assam	Dima Hasao (1), Darrang (1); (2 Districts)	2
Total	10	62 Districts	99

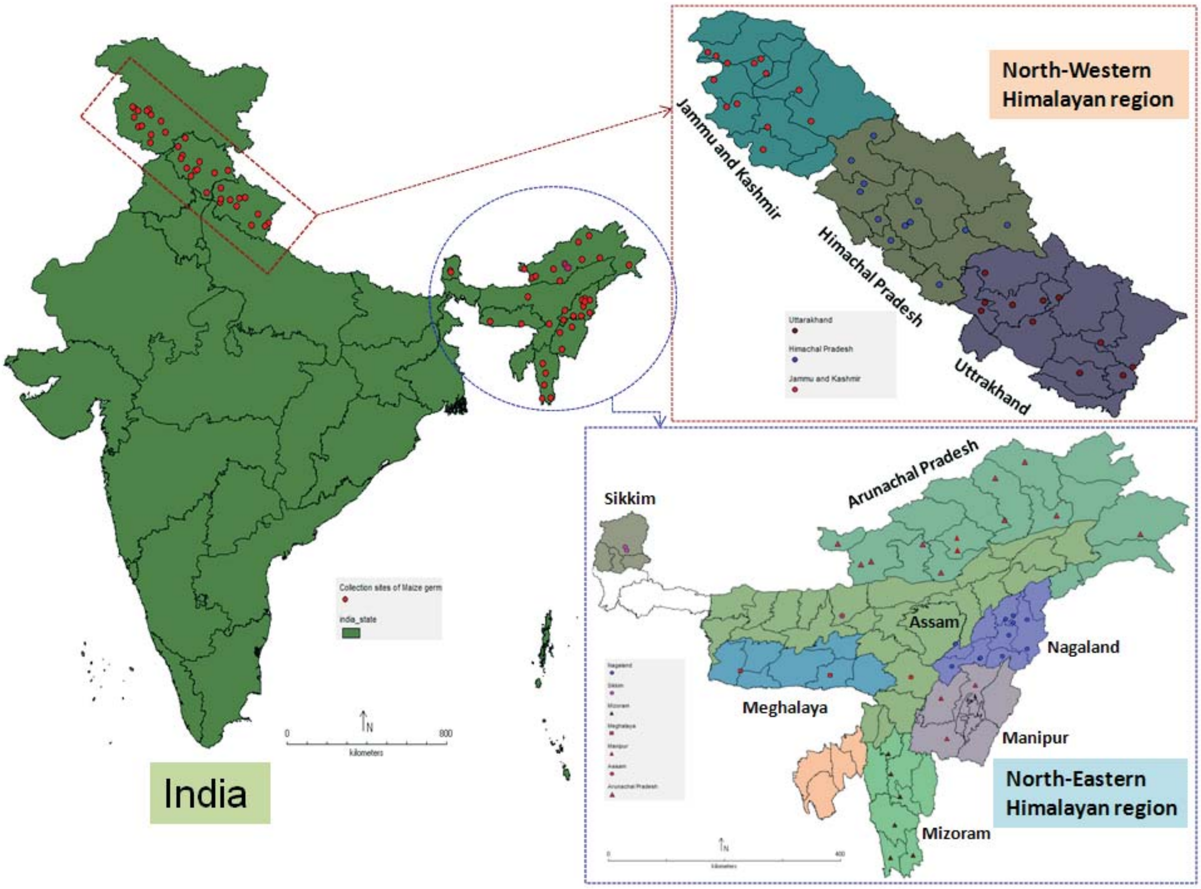

Fig. 1. Geo-referencing of maize landrace accession's collection sites located in 62 districts of 10 states of India's North-Eastern and North-Western Himalayan regions

Recommended cultural and agronomic practices were followed to raise a healthy crop.

Phenotypic Characterization

The data were recorded for 30 morphological traits following Bioversity International's descriptors for maize genetic resources (Alercia, 2011). These included 14 quantitative traits namely days to 50% tasseling (DT), days to 50% silking (DS), plant height (PH, cm), ear height (EH, cm), leaf length (LL, cm), leaf width (LW, cm), number of tassel branching (TB), number of ears per plant (EP), days to 80% maturity (DM), ear length (EL, cm), ear width (EW, cm), number of kernel rows (KR), number of kernels per row (KPR) and 100-seed weight (SW), and 16 qualitative traits *viz.*, early plant vigour, three tassel traits (texture, glume colour and glume-base colour), five leaf traits (colour, orientation, pubescence, texture and shape), silk colour, anthocyanin pigmentation, husk cover, ear shape and three kernel traits (colour, texture and shape). The morphological traits were measured on randomly chosen five plants per accession.

Statistical Analyses

Analysis of variance (ANOVA) for individual years and pooled data was carried out as per ABD using SAS 9.3 (SAS Institute, 2011) and then adjusted mean values were used for statistical analyses. The morphological traits were further analysed for mean, minimum, maximum, standard error, standard deviation, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and boxplot distribution. Pearson's correlation coefficients were calculated among all the quantitative variables using SPSS version 20 (IBM SPSS, 2020). The accessions were classified using hierarchical clustering analysis based on morphological traits. Euclidean distances were estimated and the matrix was further analyzed using Ward's method of minimum variance for generating constellation plot using JMP 14 software of SAS. Phenotypic diversity was also estimated using principal component analysis based on 14 quantitative traits. The biplot based on two principal components were also generated to depict the two-dimensional view of accession scores as well as trait variability. Shannon diversity indices (H') were calculated to study diversity in entire germplasm studied (Shannon and Weaver, 1948).

$$H' = \sum_{i=1}^{n} pi.\log_2 pi$$

where p_i is the proportion of accessions in the i^{th} class of an n-class character and n is the number of phenotypic classes for a character.

Results

Phenotypic Diversity for Quantitative Traits

Analysis of variance with pooled data for 14 different quantitative traits showed significant differences for all the traits except ear width and ear per plant (Supplementary Tables 1a-c) and revealed the presence of high extent of phenotypic variability in maize landraces accessions (Fig. 2). The germplasm characterization showed high range of variation for all the traits measured (Table 3.). Trait DT varied from 43.0 (IC077463) to 89.0 (IC130596) days after sowing with mean value of 55.9 days. DS varied from 47.7 (IC128844, IC108164) to 94.7 (IC130596) days with mean value of 58.9 days. PH ranged from 115.0 (LM-13) to 252.6 (IC447091) cm with mean value of 194.7 cm. EH varied from 59.3 (LM-14) to 159.2 (IC53885) cm with mean value

Fig. 2. Phenotypic variability in ear shape and size present in accessions from North-Western Himalayan (a-c) and North-Eastern Himalayan (d-f) regions of India

Table 3. Descriptive statistics for 14 quantitative traits analysed in 99 accessions of maize landraces and four checks based on two year's pooled data

Statistics / Trait	Range		Mean ± S.E.	Standard Deviation	Variance	PCV (%)	GCV (%)	H^2 % (broad sense)	SDI
	Min.	Maxi.							
DT	43.0	89.0	55.94 ± 0.69	7.01	49.11	12.54	11.59	53.40	0.390
DS	47.7	94.7	58.97 ± 0.71	7.25	52.59	12.31	11.43	54.62	0.370
PH	115.0	252.6	194.67 ± 2.81	28.52	813.30	14.65	13.24	55.90	0.397
EH	59.3	159.2	112.88 ± 2.10	21.34	455.47	18.92	14.13	47.21	0.411
LL	54.9	98.8	80.28 ± 0.98	9.96	99.14	12.40	9.11	46.33	0.104
LW	5.5	10.3	8.19 ± 0.09	0.88	5.20	10.64	7.73	44.19	0.470
TB	10.2	39.0	22.03 ± 0.59	6.00	36.00	27.23	15.94	54.21	0.986
EP	1.0	2.1	1.22 ± 0.03	0.28	0.08	22.67	15.59	44.26	0.779
DM	78.0	122.0	93.42 ± 0.58	5.90	34.75	6.31	4.90	53.89	0.263
EL	9.5	19.9	15.45 ± 0.17	1.68	2.82	10.87	8.98	73.86	0.385
EW	2.7	4.2	3.54 ± 0.03	0.27	0.07	7.60	5.50	70.76	0.691
KR	8.7	15.2	12.03 ± 0.12	1.23	1.52	10.24	6.71	64.93	0.950
KPR	17.0	39.3	28.23 ± 0.42	4.29	18.44	15.21	8.37	72.18	0.690
SW	12.8	31.0	23.22 ± 0.32	3.27	10.72	14.10	11.76	52.72	0.224

DT: Days to tasseling, DS: Days to silking, PH: Plant height (cm), EH: Ear height (cm), LL: Leaf length (cm), LW: Leaf width (cm), TB: Tassel branching, EP: Ears per plant, DM: Days to maturity, EL: Ear length (cm), EW: Ear width (cm), KR: Number of kernel rows, KPR: Number of kernel per row, SW: 100-Seed weight (g). PCV: Phenotypic Coefficient of Variance, GCV: Genotypic Coefficient of Variance, H^2: Heritability (broad sense), SDI: Shannon-Weaver Diversity Index

of 112.9 cm. LL varied from 54.9 (IC130596) to 98.8 (IC556413) cm with mean value of 80.3 cm, whereas LW ranged from 5.5 (IC097900) to 10.3 (PMH-1) cm with mean value of 8.2 cm. TB varied from 10.2 (IC130596) to 39.0 (IC524611) with mean value of 22.0. EP ranged from 1.0 (IC557452) to 2.1 (IC526430, IC077192) with mean value of 1.2. DM ranged from 78.0 (IC108164) to 122.0 (IC130596) days with a mean value of 93.4 days. EL showed high variation as it varied from 9.5 (IC338450) cm to 19.9 cm (IC538074) with a mean value of 15.5 cm, while EW ranged from 2.7 (IC338450) to 4.2 (IC282853) cm with mean value of 3.5 cm. KR varied from 8.7 (IC130596) to 15.2 (IC128788) with a mean value of 12.0, however, KPR displayed high range of variation from 17.0 (IC130596) to 39.3 (IC077390) with a mean value of 28.2. The seed weight ranged from 12.8 g (IC130596) to 31.0 g (PMH-1) with a mean value of 23.2 g.

The estimates of PCV and GCV with respect to 14 quantitative traits were obtained and heritability-broad sense was worked out. The estimated PCV values were higher than the GCV values for all the traits indicating greater influence of environment on the expression of traits. Higher estimates of phenotypic and genotypic coefficients were observed for tassel branching and ears per plant followed by ear height. However, low PCV and GCV were recorded for days to maturity and ear width followed by kernel rows. Broad-sense heritability estimates for assessed traits ranged between 44.19% (in leaf width) and 73.86 (in ear length) and are presented in Table 3. High heritability (>50%) were exhibited by flowering traits (days to 50% tasseling, days to 50% silking), plant height, tassel branching, days to maturity, ear length, ear width, kernel rows, kernels per row and 100-seed weight. Moderate to low (<50%) heritability estimates were shown by ear height, leaf length and width, and ear per plant. It is interesting to note that ear traits such as ear length and width, kernel rows, and kernels per row showed very high estimates of heritability. The higher values of standard deviation were found for plant height and ear height, and it was also reflected in very high estimates of variance for these traits (Table 3). Shannon-Weaver diversity indices were very high for tassel branching, ear per plant, ear width, kernels per row and kernel rows displaying the presence of very high phenotypic diversity for these traits in the landrace accessions analyzed in this study.

Boxplot Distribution of Genetic Variation

The boxplot analysis was performed to compare the variation in landrace accessions from NEH regions and NWH region for 14 quantitative traits (Fig. 3). The box showed the inter quartile range that is the box length to examine how the data was dispersed. The longer the box the more dispersed the data and the smaller the box less dispersed the data. The boxplot analysis revealed that the maize accessions from NEH region had more average values for most of the quantitative traits namely

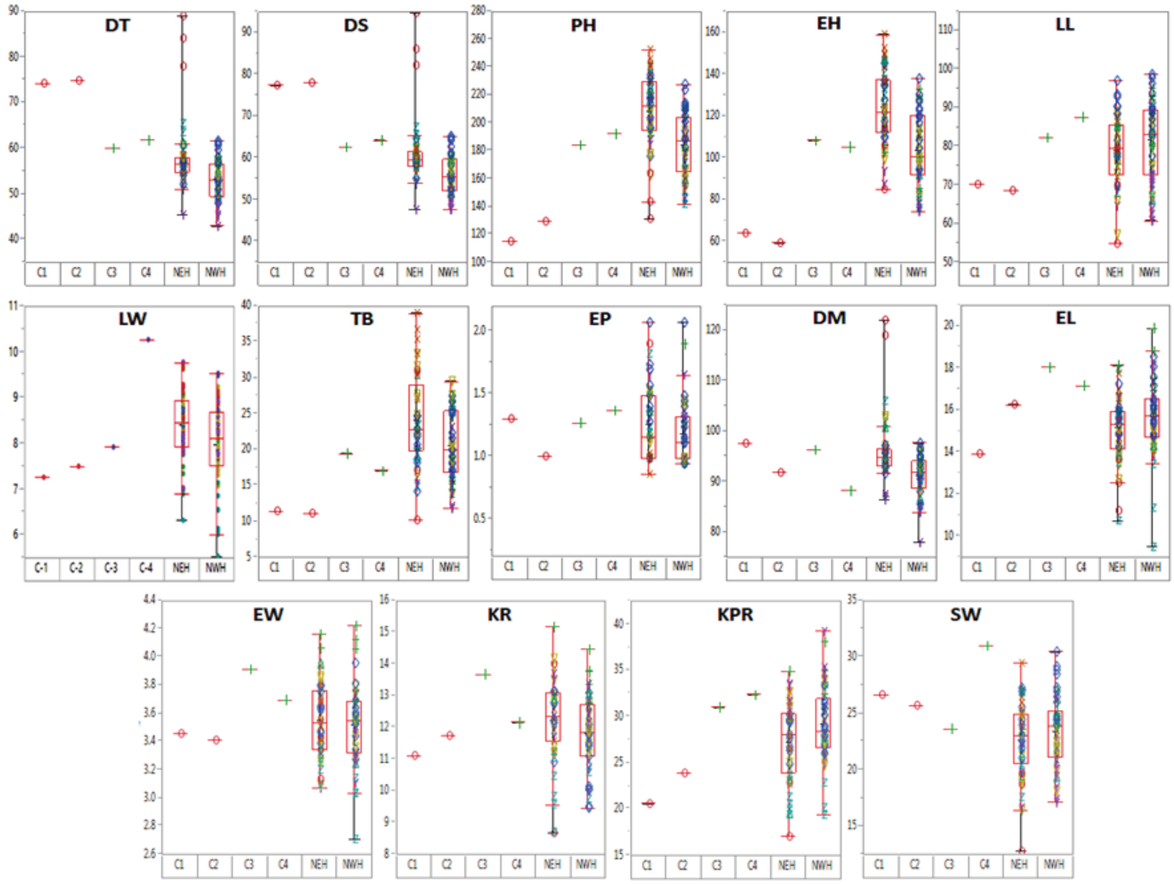

Fig. 3. Boxplot analysis depicting the differences in quartiles and mean values for 14 quantitative traits measured in 99 maize accessions from North-Eastern (50 accessions) and North-Western (49 accessions) Himalayan regions of India along with four checks

DT, DS, PH, EH, LW, TB, EP, DM and kernel KR. However, the inter quartile range, which showed the dispersal of the quantitative data, was comparatively less in most of these traits. The enter quartile range was higher for five traits namely TB, EP, EW, KPR and SW in accessions of NEH. The NWH accessions showed higher mean values for five traits such as LL, EL, EW, KPR and SW but the box length was higher for nine traits *viz*., DT, DS, PH, EH, LL, LW, EL, KR and DM. Thus, the maize landrace accessions from NWH region possessed greater morphological diversity in phenological and plant architecture traits as reflected in boxplot analysis (Fig. 3).

Associations among Quantitative Traits

The inter-relationships among 14 quantitative traits were estimated through Pearson's correlation coefficients (Supplementary Table 2). Days to tasseling (DT) had significantly positive correlations with DS (0.993) and DM (0.767). However, DT showed significantly negative correlations with EL (-0.219) and KPR (-0.399). The trait days to silking (DS) had significantly positive correlation with DM (0.779), and significantly negative correlation with KPR (-0.426). Similarly, plant height (PH) had significantly positive correlations with EH (0.895), LL (0.351), LW (0.265), TB (0.461), EL (0.453), (EW; 0.234) and SW (0.365). Ear height (EH) had significantly positive correlations with LL (0.360), LW (0.346), TB (0.447), DM (0.239), EL (0.288), EW (0.222) and SW (0.291). Leaf length (LL) showed significantly positive correlations with LW (0.533), EL (0.394), EW (0.365), KPR (0.198) and SW (0.467). However, leaf width (LW) exhibited significantly positive correlations with TB (0.227), ear per plant (EP; 0.270), EW (0.474) and kernel rows (KR; 0.251) and SW (0.285). Days to maturity (DM) showed significant negative correlations with EL (-0.217) and KPR (-0.435). Ear length (EL) had significantly positive correlations with EW (0.440), KPR (0.524) and SW (0.435). Ear width (EW) had significantly positive correlations with KR (0.528), KPR (0.356) and SW (0.450). Kernel row (KR) had positive and significant correlation with KPR (0.439).

Principle Component and Cluster Analyses

The principal component analysis (PCA) based on 14 quantitative morphological traits was performed to reduce the data set. The PCA analysis determined Eigen values of 14 morphological traits in 99 maize landraces accessions along with four checks, explained variance and cumulative variance. *Eigen values* measure the amount of variation retained by each principal component. Ten principal components contributed the major share of variance (99.95%) in maize germplasm (Supplementary Table 3). The first principal component (PC1) accounted for 78.25% of variation (Supplementary Fig. 1). In this principal component the major contributing traits toward variation were plant height, ear height, ear length and tassel branching. Second principal component (PC2) accounted for 9.99% of variation with days to 50% tasseling, days to 50% silking, days to 80% maturity are the major contributing traits. However, PC3 showed 5.59% of variation and the main contributing traits were leaf length and width, and seed weight. PC4 accounted for 2.15% of variation and days to tasseling and days to silking were the major contributing traits. PC5 contributed 1.78% of variation and tassel branching was the major contributing trait.

A hierarchical cluster analysis (HCA) was performed based on 14 quantitative variables. In order to get the best possible classification, several analyses were tested with different agglomeration methods. The agglomeration method that produced the best result was the Ward method, which provided the constellation plot (Fig. 4). This plot arranges the individuals as endpoints and each cluster join as a new point, with lines drawn that represent membership. The longer lines represent greater distance between clusters. The plot divided the collections into 8 clusters with the membership of 3, 2, 8, 20, 8, 26, 27 and 9 accessions. Mean and standard deviation estimates for each cluster groups are presented in Supplementary Table 4. Among all 8 clusters, Cluster VII was the largest cluster and II was the smallest one. Cluster I comprised of germplasm accessions having small plant height and ear height. Cluster II had accessions having late maturity, less leaf length, less tassel branching, less ear per plant, less ear length, less kernels per row with

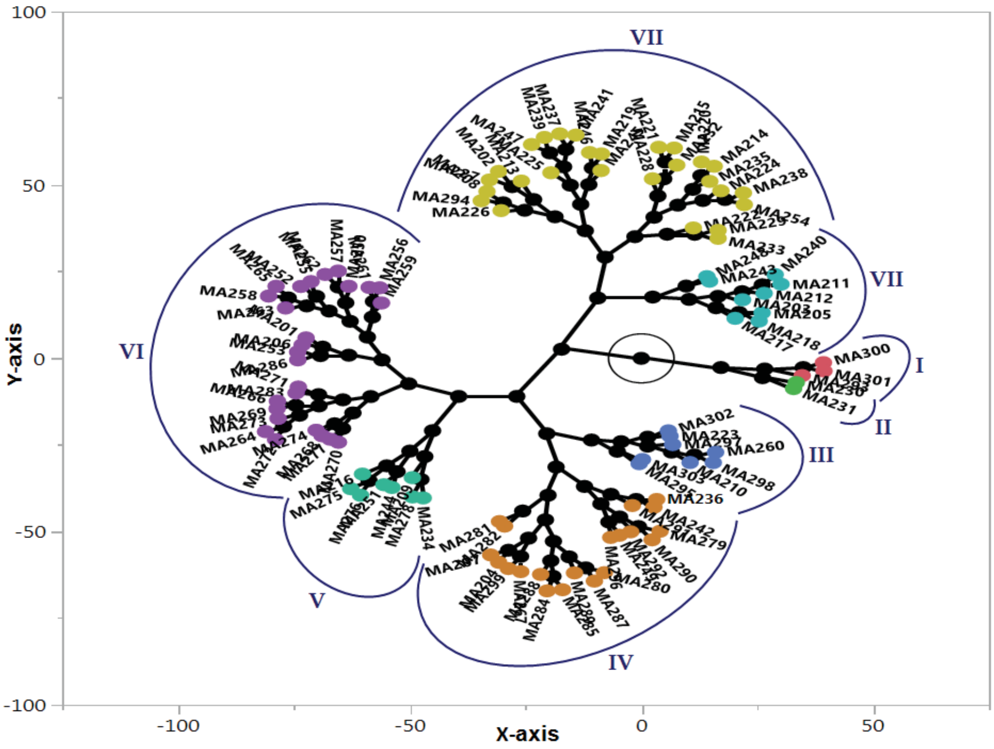

Fig. 4. Cluster analysis depicting constellation plot of maize accessions. Clusters I, II, III, IV, V, VI, VII and VIII represent different groups of maize collections

Table 4. Promising accessions selected for 14 quantitative traits based on two year's pooled data

Traits	Promising Accessions*
Day to 50% tasseling (DT)	IC077463 (MA203), IC108164 (MA227), IC128844 (MA225), IC108162 (MA226), IC077390 (MA202), IC098274 (MA218), IC381423 (MA239), IC393088 (MA240), IC278614 (MA236), IC411752 (MA241) ≤ 48 days
Day to 50% silking (DS)	IC128844 (MA225), IC108164 (MA227), IC077463 (MA203), IC108162 (MA226), IC077390 (MA202), IC098274 (MA218), IC278614 (MA236), IC381423 (MA239), IC393088 (MA240), IC411752 (MA241) ≤ 51 days
Plant height (cm) (PH)	IC447091 (MA272), IC538895 (MA266), IC524456 (MA269), IC557462 (MA274), IC083146 (MA209), IC526702 (MA283), IC538939 (MA288), IC524478 (MA273), IC447215 (MA286), IC557454 (MA287) ≥ 231 cm
Ear height (cm) (EH)	IC538895 (MA266), IC447091 (MA272), IC524456 (MA269), IC524478 (MA273), IC540252 (MA281), IC396886 (MA278), IC083146 (MA209), IC557454 (MA287), IC524611 (MA268), IC540219 (MA264) ≥ 143 cm
Leaf length (cm) (LL)	IC556413 (MA257), IC568238 (MA255), IC556430 (MA253), IC538939 (MA288), IC556406 (MA250), IC538074 (MA297), IC568279 (MA256), IC524527 (MA285), IC556415 (MA298), IC556411 (MA252) ≥ 93 cm
Leaf width (cm) (LW)	C-4(MA303), IC526764 (MA262), IC077124 (MA290), IC412888 (MA279), IC282853 (MA295), IC556415 (MA298), IC130593 (MA293), IC540252 (MA281), IC326569 (MA238), IC526436 (MA263) ≥ 9.24 cm
Tassel branching (TB)	IC524611 (MA268), IC557462 (MA274), IC419530 (MA270), IC538976 (MA277), IC524456 (MA269), IC526436 (MA263), IC128762 (MA221), IC130593 (MA293), IC526702 (MA283), IC540242 (MA271) ≥ 31
Ears per plant (EP)	IC526430 (MA289), IC077192 (MA291), IC130593 (MA293), IC282853 (MA295), IC130786 (MA234), IC545332 (MA284), IC557454 (MA287), IC526460 (MA267), IC447153 (MA280), IC077463 (MA203) ≥ 1.65
Days to 80% Maturity (DM)	IC108164 (MA227), IC077390 (MA202), IC077463 (MA203), IC469859 (MA294), IC098274 (MA218), IC338450 (MA248), IC077261 (MA201), IC108162 (MA226), IC281540 (MA247), IC077126 (MA205) ≤ 86.5 days
Ear length (cm) (EL)	IC538074 (MA297), IC097918 (MA213), IC077181 (MA206), IC077390 (MA202), IC083153 (MA210), IC556396 (MA299), C-3 (MA302), IC083146 (MA209), IC524456 (MA269), IC556430 (MA253) ≥ 17.6 cm
Ear width (cm) (EW)	IC282853 (MA295), IC083153 (MA210), IC538074 (MA297), IC128788 (MA223), IC556415 (MA298) IC556396 (MA299), IC540252 (MA281), IC538976 (MA277) C-3(MA302), IC128792 (MA224) ≥ 3.86 cm
Number of kernel rows (KR)	IC128788 (MA223), IC556415 (MA298), IC128768 (MA222), IC130605 (MA231), IC526679 (MA282), IC282853 (MA295), IC550360 (MA260), IC083125 (MA208), C-3 (MA302), IC128844 (MA225) ≥ 13.5
Number of kernels per row (KPR)	IC077390 (MA202), IC097918 (MA213), IC108162 (MA226), IC550360 (MA260), IC083153 (MA210), IC098274 (MA218), IC098165 (MA219), IC097965 (MA215), IC556415 (MA298), IC083125 (MA208) ≥ 33.6
100 seed weight (g) (SW)	C-4(MA303), IC550365 (MA261), IC526702 (MA283), IC077160 (MA292), IC077261 (MA201), IC568279 (MA256), IC077181 (MA206), IC077124 (MA290), IC083153 (MA210), IC538074 (MA297) ≥ 27.0 g

*Promising accessions were selected based on lowest 10 values for DT, DS and DM and for other traits it was top 10 entries.

high days to tasseling and silking. Cluster III comprised of accessions having high leaf length, leaf width, ear length, ear width with high kernel rows, kernels per row and medium maturity. Accessions from cluster IV having high ears per plant with medium seed weight. Cluster V had accessions having medium maturity and less kernel rows. Accessions from cluster VI having medium maturity with high plant height, ear height, tassel branching and high seed weight. Cluster VII comprised of accessions having medium plant height and medium ear height. Cluster VIII had accessions having early maturity, less leaf width, ear width along with lesser days to tasseling and silking.

Phenotypic Diversity in Qualitative Traits

Frequency distributions of 16 qualitative traits showing variability among maize landrace accessions from NEH and NWH regions of India are presented in Supplementary Fig. 2. The early plant vigour characterized the maize accessions into 3 groups namely poor (9), good (22) and very good (68) accessions. Most of the maize accessions were included in the category of very good plant vigour indicating that the majority of these accessions were selected by farmers for their robust growth habit. Most of the maize accessions (88) exhibited medium type of tassel texture (88.9%), whereas dense type was observed only in 11 accessions (11.1%). Tassel glume colour was light-purple in most of the maize accessions (51) followed by green (41) and purple (7). Tassel glume-base colour was present in 60 accessions of maize (60.6 %), while it was absent in rest. Leaf colour categorized the maize accessions into four groups and the green colored leaves were the most frequent (75.8%) followed by dark-green (18.2%) and light-green (5.1%). Yellow green leaves were present in only one landrace accession (IC393088). Most of the accessions showed the drooping type of leaf orientation (71.7%), however, 28.3% accessions showed the erect leaf type. Leaf pubescence was present in 57% accessions. It was leathery type of leaf texture present in mostly accessions (51), while the normal leaf texture was observed in 48 accessions (48.5%). Medium leaf shape was the dominant (86.9%), while broad leaves were observed in 9.09% accessions and only four accessions (4.04%) exhibited narrow leaves.

Silk colour in most of the accessions was green (87.9%), however, pink (7), purple (3) and red (2) colored silk were also recorded. Anthocyanin pigmentation was present in 51.5% accessions, whereas in 48 accessions (48.5%) the pigmentation was absent. Most of the accessions displayed yellow kernel colour (93.9%), whereas 6 accessions (6.1%) included in the other category. Maize accessions were categorized into three groups on the basis of husk cover namely poor, intermediate and good. The intermediate type of husk cover was the most frequent (64.7%) followed by poor (25.3%). In majority of maize accessions the shape of ear was observed as cylindrical (54.6% accessions), while it was conical in 38.4% accessions. Cylindrical-conical and round shaped ears were also observed in 5.05% and 2.02% accessions, respectively. Most of the accessions produced flint type of kernel texture (65.7%) followed by dent in 33.3% accessions. However, semi-flint type was present only in one accession (IC130596). Round shaped kernels were the most frequent kernel shape found in 58.6% accessions of maize, whereas the indented kernel shape was observed in 41 maize accessions (41.4%).

Discussion

Maize (*Z. mays*) is an important cereal crop with the highest genetic diversity in the form of landraces, open pollinated varieties, composites, hybrids and crop wild relatives including progenitor species. The maize genome (2.3 Gb) consisting of ~85% repeated sequences mainly of hundreds of families of transposable elements and duplicated genes, is thought to be an ancient segmental allotetraploid but functions as genetically diploid (Gaut and Doebley, 1997; Gaut *et al*., 2000; Schnable *et al*., 2009). Chromosomal behaviour analysis in monosomics revealed the presence of duplicated chromosome segments in maize genome (Yadav *et al*., 2009). Although maize was first domesticated in Mexico, its landraces are widely distributed across the continents (Sachan, 1991; Matsuoka *et al*., 2002).

Maize varieties being cultivated in Indian subcontinent are early in maturity with yellow to light yellow kernels. These varieties had undergone natural as well as farmer's selection during past five centuries. The landrace materials had adapted to local niches due to conservation and selection by local people's inhabiting different tribal regions inaccessible to urban communities (Singh, 1977). These man-made selections and conservation of landraces through religious customs and rituals had resulted in high genetic drift and consequently development of geographically isolated populations of landraces mainly in NEH and NWH high-lands of India. These man-made selections for centuries have resulted in the high extent of morphological variations in plant, tassel and ear traits in these maize landraces of NEH and NWH regions of India (Prasanna and Sharma, 2005). Numerous expeditions were undertaken for germplasm collections in the past (Grant and Wellhausen, 1955; Ono and Suzuki, 1956; Dhawan, 1964; Thapa, 1966) and reported wealth of information on the landraces and the presence of high extent of morphological diversity in the NEH region. They also compared the diversity of maize races present in NEH region with that of landrace germplasm found in plain areas of India. In contrast to the Indo-Gangetic plains, extensive variability for plant and ear characteristics (multiple cobs per plant) was reported in NEH region and NWH region (Anderson, 1945; Stonor and Anderson, 1949; Singh, 1977).

In the backdrop of such an extensive diversity of maize landraces in NEH and NWH regions of India, the plant exploration and germplasm collection teams of ICAR-NBPGR visited these regions and periodically collected diverse accessions of maize landraces (PGR portal, http://www.nbpgr. ernet.in:8080 /PGRPortal). In view of the available germplasm of maize landraces from NEH and NWH region in our national gene bank, we selected 99 accessions from 62 districts of 10 states located in maize biodiversity hotspots for phenotypic characterization of maize landraces. The high extent of morphological variation, as evident by high Shannon-Weaver diversity indices, was recorded for tassel branching (0.99), kernel rows (0.95), ear per plant (0.78), ear width (0.69), and kernel per row (0.69). However, moderate diversity was recorded in quantitative traits such as ear height (0.41) and leaf width (0.47). Most of the qualitative traits namely early plant vigour (0.79), tassel glume colour (0.89), tassel glume-base colour (0.67), Leaf colour (0.72), leaf orientation (0.75), leaf pubescence (0.68), leaf texture (0.69), anthocyanin pigmentation (0.69), ear shape (0.98), husk cover (0.85), kernel texture (0.69) and kernel shape (0.68) displayed very high level of phenotypic variation as revealed by Shannon-Weaver diversity indices.

Several studies had reported the existence of high phenotypic variability in maize landraces across the globe including Asia (Ilarslan *et al*., 2002; Wei *et al*., 2009; Sharma *et al*., 2010; Kumar *et al*., 2015; Kumari *et al*., 2017), Africa (Belalia *et al*., 2018; Nelimor *et al*., 2019; Kasoma *et al*., 2020), Europe (Gouesnard *et al*., 1997; Rebourg *et al*., 2001; Hartings *et al*., 2008) and Central and South America (Bracco *et al*., 2009; Salazar *et al*., 2016; Osorio-Saenz *et al*., 2019). Ilarslan *et al.* (2002) assessed the genetic variability among 32 Turkish populations, mainly of flint and dent type races, based on 25 morphological and agronomic traits. They reported total variance ranged from 17.17% in kernel length to 82.75% in tassel length. Wei *et al.* (2009) evaluated phenotypic and genetic diversity of 102 maize landraces from Hubei province of South-West China based on 12 phenotypic characters. The landraces contained greater extent of variations for earliness, plant architecture, and ear and kernel characteristics. They suggested that the presence of abundant genetic diversity and favourable genes accumulated within these landraces should be used in maize breeding programmes.

In India, Sharma *et al.* (2010) reported phenotypically highly diverse maize landraces from NEH region and the majority of landraces analyzed were from Sikkim state including ‘Sikkim primitive’. This study revealed that Sikkim primitive race, which had unique prolificacy (produced 5-9 ears on a single stalk), clearly separated from rest of the accessions. PCA showed two principal components describing 90% of total variation and 100 seed weight, ear length and diameter, kernels per ear and flowering behaviour were the most discriminating traits. However, in our study the Sikkim primitive and similar types of landraces were not included and hence number of ear per plant was less (1.0-2.1 ears/plant) as compared to Sharma *et al.* (2010). Kumar *et al.* (2015) evaluated 57 accessions of maize landraces from NWH region mainly from Himachal and Jammu and Kashmir using 17 agro-morphological and quality traits. In this study, cluster analysis revealed four groups and the accession from Jammu and Kashmir were grouped into cluster-I. PCA revealed that plant height, ear height, leaf length and quality traits (protein, oil, sugar and starch) were the major contributing traits towards diversity. They also selected three accessions based on quality trait for future maize breeding programme. Similarly, Thakur *et al.* (2017) reported high genetic diversity in 48 maize genotypes including 11 local maize germplasm from Himachal Pradesh and two germplasm lines from Sikkim based on 11 morphological traits. Kumari *et al.* (2017) characterized 75 diverse maize accessions collected from Nagaland and Manipur states of NEH region using 12 quantitative characters and reported significant morphological variability among these accessions. Cluster analysis grouped these accessions into five clusters and PCA showed that first two PCs contributed more than 50% of phenotypic variation. Plant height, ear height, ear width, number of kernels per row and kernel rows are major contributing traits towards phenotypic diversity.

The descriptive statistics revealed that our results on plant phenology (days to tasseling, days to silking, plant height, ear height, leaf length and leaf width) and ear traits (ear length, kernels per row and 100 seed weight) corroborate with the findings of Sharma *et al.* (2010), Salazar *et al.* (2016), Kumar *et al.* (2015) and Kumari *et al.* (2017) except minor variations in the range and means of ear height, plant height and seed weight. These differences in the quantitative traits could be explained due to presence of environmental, genotype × environmental effects, and the genetic makeup differences in the landraces materials analyzed in these studies. The presence of very high positive correlations between flowering (DT and DS, r=0.99) and maturity (DM and DT, r=0.77; DM and DS, r = 0.78) traits, and between plant and ear height (r=0.90) in our study indicates that the selection for one trait would simultaneously improve the correlated traits. Our results on correlation studies confirm the findings of Belalia *et al.* (2019) who reported highly positive correlations between PH and EH (r=0.95), and between days to anthesis and silking (r=0.94). Presence of linkage drag in traits showing significantly higher negative correlations would require breaking up of these negative correlations for simultaneous improvement in these traits for example kernels per row showed strong negative correlation with flowering traits (days to tasseling and silking) and maturity. Similarly, ear length and width, kernel rows and 100-seed weight also exhibited weak negative correlations with the flowering and maturity traits. The plant morphological traits namely leaf length, leaf width and tassel branching showed significant positive correlation with plant height and ear height indicating the presence of linked genes encoding for these different phenotypic traits (Cömertpay *et al*., 2012).

Moreover, our results are in good agreement with previous studies documenting the extensive variations for morphological traits in maize landraces collected from different parts of the world (Rebourg *et al*., 2001; Pressoir and Berthaud, 2004; Buckler *et al*., 2006;

Hartings *et al*., 2008; Warburton *et al*., 2008). The strong point of this research is the comparative study of phenotypic variability present in 49 accessions of maize landraces from NWH region with that of 50 accessions from NEH region of India using boxplot analysis. We found that the maize landrace accessions from NWH region possessed greater morphological diversity in plant phenology and architecture traits namely days to tasseling and silking, plant height, ear height, leaf length and width, ear length, kernel rows and days to maturity. However, the accessions of NEH region showed higher variability for tassel branching, ears per plant, ear width, kernels per row and 100-seed weight. Thus the maize accessions of NWH region possessed larger morphological diversity as compared to accessions from NEH region. Similar findings of presence of enormous diversity for plant, tassel and ear characteristics in the NEH and some parts of NWH region were also reported by earlier researchers (Dhawan, 1964; Thapa, 1966; Singh, 1977; Sharma and Prasanna, 2005; Prasanna 2010, 2012). Based on the range of variation in maize landrace accessions for different quantitative traits, we have identified 10 promising maize accessions for individual trait (Table 4). These promising accessions could be the valuable sources for genetic diversity of desirable traits for maize breeding programmes.

Conclusions

Genetic diversity is vital for genetic improvement to enhance production and productivity of maize crop. The crop genetic resources especially the landrace germplasm containing specific adaptation genes including desirable morphological and quality traits are invaluable sources of genetic diversity. In this study, we assessed morphological diversity in 99 maize landrace accessions collected from 10 different states of India located in biodiversity hotspots in NEH and NWH regions. The presence of high level of genetic variation for most of morphological traits in the landrace accessions provides an opportunity for their utilization in pre-breeding programmes for widening the primary genepool of maize and direct use as a resource for development of genetically diverse inbred lines for heterotic hybrid development in maize.

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*Supplementary Table or Figure mentioned in the article are available in the online version.

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